

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(i) APPLICANT: Genentech, Inc.
Hsei, Vanessa
Koumenis, Iphigenia
Leong, Steven R.
10 Presta, Leonard G.
Shahrokh, Zahra
Zapata, Gerardo A.

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(ii) TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
Humanized Anti-IL-8 Monoclonal Antibodies

(iii) NUMBER OF SEQUENCES: 72

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(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
25 (F) ZIP: 94080

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
30 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
35 (B) FILING DATE: 20-Feb-1998
(C) CLASSIFICATION:

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(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Love, Richard B.
40 (B) REGISTRATION NUMBER: 34,659
(C) REFERENCE/DOCKET NUMBER: P1085R3PCT

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(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650/225-5530
45 (B) TELEFAX: 650/952-9881

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs
50 (B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGTCCAACGTGTTTCAGGACG CC 22

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGCTGCTCA TGCTGTAGGT GC 22

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAAGTTGATG TCTTGTGAGT GGC 23

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCATCCTAGA GTCACCGAGG AGCC 24

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CACTGGCTCA GGGAAATAAC CC 22

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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GGAGAGCTGG GAAGGTGTGC AC 22

(2) INFORMATION FOR SEQ ID NO:7:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACAAACGCGT ACGCTGACAT CGTCATGACC CAGTC 35

15 (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: Nucleic Acid
 20 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

25 ACAAACGCGT ACGCTGATAT TGTCATGACT CAGTC 35

(2) INFORMATION FOR SEQ ID NO:9:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

40 ACAAACGCGT ACGCTGACAT CGTCATGACA CAGTC 35

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 45 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCTCTTCGAA TGGTGGGAAG ATGGATACAG TTGGTGTC 37

55 (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 60 (D) TOPOLOGY: Linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGATGGGCCC GGATAGACCG ATGGGGCTGT TGTTTTGGC 39

5 (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: Nucleic Acid
 10 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

15

CGATGGGCCC GGATAGACTG ATGGGGCTGT CGTTTTGGC 39

(2) INFORMATION FOR SEQ ID NO:13:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGATGGGCCC GGATAGACGG ATGGGGCTGT TGTTTTGGC 39

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(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 35 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CGATGGGCCC GGATAGACAG ATGGGGCTGT TGTTTTGGC 39

45 (2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 50 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

55 CGATGGGCCC GGATAGACTG ATGGGGCTGT TGTTTTGGC 39

(2) INFORMATION FOR SEQ ID NO:16:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 369 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

5 GACATTGTCA TGACACAGTC TCAAAAATTC ATGTCCACAT CAGTAGGAGA 50
 CAGGGTCAGC GTCACCTGCA AGGCCAGTCA GAATGTGGGT ACTAATGTAG 100
 10 CCTGGTATCA ACAGAAACCA GGGCAATCTC CTAAAGCACT GATTTACTCG 150
 TCATCCTACC GGTACAGTGG AGTCCCTGAT CGCTTCACAG GCAGTGGATC 200
 TGGGACAGAT TTTACTCTCA CCATCAGCCA TGTGCAGTCT GAAGACTTGG 250
 15 CAGACTATTT CTGTCAGCAA TATAACATCT ATCCTCTCAC GTTCGGTCCT 300
 GGGACCAAGC TGGAGTTGAA ACGGGCTGAT GCTGCACCAC CAACTGTATC 350
 20 CATCTTCCCA CCATTGAA 369

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 123 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

30 Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val
 1 5 10 15
 35 Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly
 20 25 30
 Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
 35 40 45
 40 Ala Leu Ile Tyr Ser Ser Ser Tyr Arg Tyr Ser Gly Val Pro Asp
 50 55 60
 Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
 65 70 75
 45 Ser His Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln
 80 85 90
 50 Tyr Asn Ile Tyr Pro Leu Thr Phe Gly Pro Gly Thr Lys Leu Glu
 95 100 105
 Leu Lys Arg Ala Asp Ala Ala Pro Pro Thr Val Ser Ile Phe Pro
 110 115 120
 55 Pro Phe Glu
 123

(2) INFORMATION FOR SEQ ID NO:18:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 417 base pairs
 (B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

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TTCTATTGCT ACAAACGCGT ACGCTGAGGT GCAGCTGGTG GAGTCTGGGG 50
GAGGCTTAGT GCCGCCTGGA GGGTCCCTGA AACTCTCCTG TGCAGCCTCT 100
GGATTCATAT TCAGTAGTTA TGGCATGTCT TGGGTTCGCC AGACTCCAGG 150
CAAGAGCCTG GAGTTGGTCG CAACCATTAA TAATAATGGT GATAGCACCT 200
ATTATCCAGA CAGTGTGAAG GGCCGATTCA CCATCTCCCG AGACAATGCC 250
AAGAACACCC TGTACCTGCA AATGAGCAGT CTGAAGTCTG AGGACACAGC 300
CATGTTTTAC TGTGCAAGAG CCCTCATTAG TTCGGCTACT TGGTTTGGTT 350
ACTGGGGCCA AGGGA CTCTG GTCAGTGTCT CTGCAGCCAA AACAACAGCC 400
CCATCTGTCT ATCCGGG 417

25 (2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Pro Pro Gly
35 1 5 10 15
Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser
20 25 30
Ser Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Gly Lys Ser Leu
40 35 40 45
Glu Leu Val Ala Thr Ile Asn Asn Asn Gly Asp Ser Thr Tyr Tyr
50 55 60
Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
65 70 75
Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp
50 80 85 90
Thr Ala Met Phe Tyr Cys Ala Arg Ala Leu Ile Ser Ser Ala Thr
95 100 105
Trp Phe Gly Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
55 110 115 120
Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro
125 130

60

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ACAAACGCGT ACGCTGATAT CGTCATGACA G 31

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCAGCATCAG CTCTTCGAAG CTCCAGCTTG G 31

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCACTAGTAC GCAAGTTCAC G 21

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GATGGGCCCT TGGTGGAGGC TGCAGAGACA GTG 33

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 714 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATGAAGAAGA ATATCGCATT TCTTCTTGCA TCTATGTTG TTTTTTCTAT 50

TGCTACAAAC GCGTACGCTG ATATCGTCAT GACACAGTCT CAAAAATTCA 100
 TGTCCACATC AGTAGGAGAC AGGGTCAGCG TCACCTGCAA GGCCAGTCAG 150
 5 AATGTGGGTA CTAATGTAGC CTGGTATCAA CAGAAACCAG GGCAATCTCC 200
 TAAAGCACTG ATTTACTCGT CATCCTACCG GTACAGTGGA GTCCCTGATC 250
 10 GCTTCACAGG CAGTGGATCT GGGACAGATT TCACTCTCAC CATCAGCCAT 300
 GTGCAGTCTG AAGACTTGGC AGACTATTTT TGTGAGCAAT ATAACATCTA 350
 TCCTCTCACG TTCGGTCCTG GGACCAAGCT GGAGCTTCGA AGAGCTGTGG 400
 15 CTGCACCATC TGTCTTCATC TTCCCGCCAT CTGATGAGCA GTTGAAATCT 450
 GGAAGTCTT CTGTTGTGTG CCTGCTGAAT AACTTCTATC CCAGAGAGGC 500
 20 CAAAGTACAG TGGAAGGTGG ATAACGCCCT CCAATCGGGT AACTCCCAGG 550
 AGAGTGTCAC AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC 600
 ACCCTGACGC TGAGCAAAGC AGACTACGAG AAACACAAAG TCTACGCCTG 650
 25 CGAAGTCACC CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTTCAACA 700
 GGGGAGAGTG TTAA 714

30 (2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
 (B) TYPE: Amino Acid
 35 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

40	Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	1	5	10	15
	Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Asp	Ile	Val	Met	Thr	Gln	Ser	20	25	30	
45	Gln	Lys	Phe	Met	Ser	Thr	Ser	Val	Gly	Asp	Arg	Val	Ser	Val	Thr	35	40	45	
	Cys	Lys	Ala	Ser	Gln	Asn	Val	Gly	Thr	Asn	Val	Ala	Trp	Tyr	Gln	50	55	60	
50	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Ala	Leu	Ile	Tyr	Ser	Ser	Ser	65	70	75	
55	Tyr	Arg	Tyr	Ser	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	80	85	90	
	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	His	Val	Gln	Ser	Glu	Asp	95	100	105	
60	Leu	Ala	Asp	Tyr	Phe	Cys	Gln	Gln	Tyr	Asn	Ile	Tyr	Pro	Leu	Thr	110	115	120	

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	Phe	Gly	Pro	Gly	Thr	Lys	Leu	Glu	Leu	Arg	Arg	Ala	Val	Ala	Ala	
					125					130					135	
5	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	
					140					145					150	
	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	
					155					160					165	
10	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	
					170					175					180	
	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	
					185					190					195	
15	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	
					200					205					210	
	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	
20					215					220					225	
	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys				
					230					235		237				

25 (2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 756 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

35	ATGAAAAAGA	ATATCGCATT	TCTTCTTGCA	TCTATGTTCTG	TTTTTCTAT	50
	TGCTACAAAC	GCGTACGCTG	AGGTGCAGCT	GGTGGAGTCT	GGGGGAGGCT	100
40	TAGTGCCGCC	TGGAGGGTCC	CTGAAACTCT	CCTGTGCAGC	CTCTGGATTCT	150
	ATATTTCAGTA	GTTATGGCAT	GTCTTGGGTT	CGCCAGACTC	CAGGCAAGAG	200
	CCTGGAGTTG	GTCGCAACCA	TTAATAATAA	TGGTGATAGC	ACCTATTATC	250
45	CAGACAGTGT	GAAGGGCCGA	TTCACCATCT	CCCGAGACAA	TGCCAAGAAC	300
	ACCCTGTACC	TGCAAATGAG	CAGTCTGAAG	TCTGAGGACA	CAGCCATGTT	350
50	TTACTGTGCA	AGAGCCCTCA	TTAGTTCGGC	TACTTGGTTT	GGTTACTGGG	400
	GCCAAGGGAC	TCTGGTCACT	GTCTCTGCAG	CCTCCACCAA	GGGCCCATCG	450
	GTCTTCCCCC	TGGCACCCCTC	CTCCAAGAGC	ACCTCTGGGG	GCACAGCGGC	500
55	CCTGGGCTGC	CTGGTCAAGG	ACTACTTCCC	CGAACCGGTG	ACGGTGTCTGT	550
	GGAACCTCAGG	CGCCCTGACC	AGCGGCGTGC	ACACCTTCCC	GGCTGTCCTA	600
60	CAGTCCTCAG	GACTCTACTC	CCTCAGCAGC	GTGGTGACCG	TGCCCTCCAG	650
	CAGCTTGGGC	ACCCAGACCT	ACATCTGCAA	CGTGAATCAC	AAGCCCAGCA	700

ACACCAAGGT GGACAAGAAA GTTGAGCCCA AATCTTGTGA CAAAACTCAC 750

ACATGA 756

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(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 251 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

15	Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	1	5	10	15
	Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Glu	Val	Gln	Leu	Val	Glu	Ser	20	25	30	
20	Gly	Gly	Gly	Leu	Val	Pro	Pro	Gly	Gly	Ser	Leu	Lys	Leu	Ser	Cys	35	40	45	
	Ala	Ala	Ser	Gly	Phe	Ile	Phe	Ser	Ser	Tyr	Gly	Met	Ser	Trp	Val	50	55	60	
25	Arg	Gln	Thr	Pro	Gly	Lys	Ser	Leu	Glu	Leu	Val	Ala	Thr	Ile	Asn	65	70	75	
30	Asn	Asn	Gly	Asp	Ser	Thr	Tyr	Tyr	Pro	Asp	Ser	Val	Lys	Gly	Arg	80	85	90	
	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	95	100	105	
35	Met	Ser	Ser	Leu	Lys	Ser	Glu	Asp	Thr	Ala	Met	Phe	Tyr	Cys	Ala	110	115	120	
40	Arg	Ala	Leu	Ile	Ser	Ser	Ala	Thr	Trp	Phe	Gly	Tyr	Trp	Gly	Gln	125	130	135	
	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala	Ala	Ser	Thr	Lys	Gly	Pro	Ser	140	145	150	
45	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	155	160	165	
	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	170	175	180	
50	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	185	190	195	
	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	200	205	210	
55	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	215	220	225	
60	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	230	235	240	

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Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr
245 250 251

(2) INFORMATION FOR SEQ ID NO:28:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

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(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

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CCAATGCATA CGCTGACATC GTGATGACCC AGACCCC 37

(2) INFORMATION FOR SEQ ID NO:29:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCAATGCATA CGCTGATATT GTGATGACTC AGACTCC 37

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(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: Nucleic Acid

35

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

40

CCAATGCATA CGCTGACATC GTGATGACAC AGACACC 37

(2) INFORMATION FOR SEQ ID NO:31:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

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(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

55

AGATGTCAAT TGCTCACTGG ATGGTGGGAA GATGG 35

(2) INFORMATION FOR SEQ ID NO:32:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

5 CAAACGCGTA CGCTGAGATC CAGCTGCAGC AG 32

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 32 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CAAACGCGTA CGCTGAGATT CAGCTCCAGC AG 32

20 (2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 391 base pairs
 (B) TYPE: Nucleic Acid
 25 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

30 GATATCGTGA TGACACAGAC ACCACTCTCC CTGCCTGTCA GTCTTGGAGA 50
 TCAGGCCTCC ATCTCTTGCA GATCTAGTCA GAGCCTTGTA CACGGTATTG 100
 35 GAAACACCTA TTTACATTGG TACCTGCAGA AGCCAGGCCA GTCTCCAAAG 150
 CTCCTGATCT ACAAAGTTTC CAACCGATTT TCTGGGGTCC CAGACAGGTT 200
 CAGTGGCAGT GGATCAGGGA CAGATTTTAC ACTCAGGATC AGCAGAGTGG 250
 40 AGGCTGAGGA TCTGGGACTT TATTTCTGCT CTCAAAGTAC ACATGTTCCG 300
 CTCACGTTTC GTGCTGGGAC CAAGCTGGAG CTGAAACGGG CTGATGCTGC 350
 45 ACCAACTGTA TCCATCTTCC CACCATCCAG TGAGCAATTG A 391

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 131 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

55 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu
 1 5 10 15
 60 Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val
 20 25 30
 His Gly Ile Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro

	35	40	45
	Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe		
	50	55	60
5	Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp		
	65	70	75
	Phe Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Leu		
10	80	85	90
	Tyr Phe Cys Ser Gln Ser Thr His Val Pro Leu Thr Phe Gly Ala		
	95	100	105
15	Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala Pro Thr Val		
	110	115	120
	Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Lys		
	125	130 131	

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAGATTCAGC TGCAGCAGTC TGGACCTGAG CTGATGAAGC CTGGGGCTTC 50

AGTGAAGATA TCCTGCAAGG CTTCTGGTTA TTCATTAGT AGCCACTACA 100

TGCACTGGGT GAAGCAGAGC CATGGAAGA GCCTTGAGTG GATTGGCTAC 150

ATTGATCCTT CCAATGGTGA AACTACTTAC AACCAGAAAT TCAAGGGCAA 200

GGCCACATTG ACTGTAGACA CATCTTCCAG CACAGCCAAC GTGCATCTCA 250

GCAGCCTGAC ATCTGATGAC TCTGCAGTCT ATTTCTGTGC AAGAGGGGAC 300

TATAGATACA ACGGCGACTG GTTTTTCGAT GTCTGGGGCG CAGGGACCAC 350

GGTCACCGTC TCCTCCGCCA AAACCGACAG CCCCATCGGT CTATCCGGGC 400

CCATC 405

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys Pro Gly

1 5 10 15

Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Ser

	20	25	30
	Ser His Tyr Met His Trp Val Lys Gln	Ser His Gly Lys Ser Leu	
	35	40	45
5	Glu Trp Ile Gly Tyr Ile Asp Pro Ser Asn	Gly Glu Thr Thr Tyr	
	50	55	60
10	Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu	Thr Val Asp Thr Ser	
	65	70	75
	Ser Ser Thr Ala Asn Val His Leu Ser Ser	Leu Thr Ser Asp Asp	
	80	85	90
15	Ser Ala Val Tyr Phe Cys Ala Arg Gly Asp	Tyr Arg Tyr Asn Gly	
	95	100	105
	Asp Trp Phe Phe Asp Val Trp Gly Ala Gly	Thr Thr Val Thr Val	
20	110	115	120
	Ser Ser Ala Lys Thr Asp Ser Pro Ile Gly	Leu Ser Gly Pro Ile	
	125	130	135

(2) INFORMATION FOR SEQ ID NO:38:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

30

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

35

CTTGGTGGAG GCGGAGGAGA CG 22

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GAAACGGGCT GTTGCTGCAC CAACTGTATT CATCTTCC 38

50

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: Nucleic Acid

55

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

60

GTCACCGTCT CCTCCGCCTC CACCAAGGGC C 31

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 729 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Double
 (D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATGAAGAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTTTCTAT 50
 TGCTACAAAT GCATACGCTG ATATCGTGAT GACACAGACA CCACTCTCCC 100
 15 TGCCTGTCAG TCTTGGAGAT CAGGCCTCCA TCTCTTGCA GATCTAGTCAG 150
 AGCCTTGTAC ACGGTATTGG AAACACCTAT TTACATTGGT ACCTGCAGAA 200
 20 GCCAGGCCAG TCTCCAAAGC TCCTGATCTA CAAAGTTTCC AACCGATTTT 250
 CTGGGGTCCC AGACAGGTTC AGTGGCAGTG GATCAGGGAC AGATTTTACA 300
 CTCAGGATCA GCAGAGTGGA GGCTGAGGAT CTGGGACTTT ATTTCTGCTC 350
 25 TCAAAGTACA CATGTTCCGC TCACGTTCCG TGCTGGGACC AAGCTGGAGC 400
 TGAAACGGGC TGTGCTGCA CCAACTGTAT TCATCTTCCC ACCATCCAGT 450
 30 GAGCAATTGA AATCTGGAAC TGCCTCTGTT GTGTGCCTGC TGAATAACTT 500
 CTATCCCAGA GAGGCCAAAG TACAGTGGA GGTGGATAAC GCCCTCCAAT 550
 CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600
 35 TACAGCCTCA GCAGCACCT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650
 CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGCCTGAGC TCGCCCGTCA 700
 40 CAAAGAGCTT CAACAGGGGA GAGTGTTAA 729

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 242 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
 1 5 10 15
 Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Val Met Thr Gln Thr
 55 20 25 30
 Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser
 35 40 45
 60 Cys Arg Ser Ser Gln Ser Leu Val His Gly Ile Gly Asn Thr Tyr
 50 55 60

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	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	
					65					70					75	
5	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	
					80					85					90	
	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Arg	Ile	Ser	Arg	
					95					100					105	
10	Val	Glu	Ala	Glu	Asp	Leu	Gly	Leu	Tyr	Phe	Cys	Ser	Gln	Ser	Thr	
					110					115					120	
	His	Val	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys	
15					125					130					135	
	Arg	Ala	Val	Ala	Ala	Pro	Thr	Val	Phe	Ile	Phe	Pro	Pro	Ser	Ser	
					140					145					150	
20	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	
					155					160					165	
	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	
					170					175					180	
25	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	
					185					190					195	
	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	
30					200					205					210	
	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	
					215					220					225	
	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	
35					230					235					240	
	Glu	Cys														
		242														

40 (2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 762 base pairs
(B) TYPE: Nucleic Acid
45 (C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

50 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCTG TTTTCTCTAT 50
TGCTACAAAC GCGTACGCTG AGATTCAGCT GCAGCAGTCT GGACCTGAGC 100
55 TGATGAAGCC TGGGGCTTCA GTGAAGATAT CCTGCAAGGC TTCTGGTTAT 150
TCATTACAGTA GCCACTACAT GCACTGGGTG AAGCAGAGCC ATGGAAAGAG 200
CCTTGAGTGG ATTGGCTACA TTGATCCTTC CAATGGTGAA ACTACTTACA 250
60 ACCAGAAATT CAAGGGCAAG GCCACATTGA CTGTAGACAC ATCTTCCAGC 300

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ACAGCCAACG TGCATCTCAG CAGCCTGACA TCTGATGACT CTGCAGTCTA 350
 TTTCTGTGCA AGAGGGGACT ATAGATACAA CGGCGACTGG TTTTTCGATG 400
 5 TCTGGGGCGC AGGGACCACG GTCACCGTCT CCTCCGCCTC CACCAAGGGC 450
 CCATCGGTCT TCCCCCTGGC ACCCTCCTCC AAGAGCACCT CTGGGGGCAC 500
 AGCGGGCCCTG GGCTGCCTGG TCAAGGACTA CTTCCCCGAA CCGGTGACGG 550
 10 TGTCGTGGAA CTCAGGCGCC CTGACCAGCG GCGTGCACAC CTTCCCGGCT 600
 GTCCTACAGT CCTCAGGACT CTACTCCCTC AGCAGCGTGG TGACCGTGCC 650
 15 CTCCAGCAGC TTGGGCACCC AGACCTACAT CTGCAACGTG AATCACAAGC 700
 CCAGCAACAC CAAGGTGGAC AAGAAAGTTG AGCCCAAATC TTGTGACAAA 750
 ACTCACACAT GA 762

20

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 253 amino acids
 25 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

30 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
 1 5 10 15
 Ser Ile Ala Thr Asn Ala Tyr Ala Glu Ile Gln Leu Gln Gln Ser
 20 25 30
 35 Gly Pro Glu Leu Met Lys Pro Gly Ala Ser Val Lys Ile Ser Cys
 35 40 45
 Lys Ala Ser Gly Tyr Ser Phe Ser Ser His Tyr Met His Trp Val
 40 50 55 60
 Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly Tyr Ile Asp
 65 70 75
 45 Pro Ser Asn Gly Glu Thr Thr Tyr Asn Gln Lys Phe Lys Gly Lys
 80 85 90
 Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Asn Val His
 95 100 105
 50 Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys Ala
 110 115 120
 Arg Gly Asp Tyr Arg Tyr Asn Gly Asp Trp Phe Phe Asp Val Trp
 55 125 130 135
 Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly
 140 145 150
 60 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
 155 160 165

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	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu
					170					175					180
5	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val
					185					190					195
	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu
					200					205					210
10	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr
					215					220					225
	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp
					230					235					240
15	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr		
					245					250			253		

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

	Asp	Ile	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Pro	Val	Ser	Leu
	1				5					10					15
30	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val
					20					25					30
	His	Gly	Ile	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro
35					35					40					45
	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Tyr	Lys	Val	Ser	Asn	Arg
					50					55					60
40	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Asp	Ser	Gly	Ser	Gly	Thr
					65					70					75
	Asp	Phe	Thr	Leu	Arg	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly
					80					85					90
45	Leu	Tyr	Phe	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Leu	Thr	Phe	Gly
					95					100					105
	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys	Arg						
50					110				114						

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val
	1				5					10					15

Gly Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Leu Val
 20 25 30
 5 His Gly Ile Gly Asn Thr Tyr Leu His Trp Tyr Gln Gln Lys Pro
 35 40 45
 Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Lys Val Ser Asn Arg
 50 55 60
 10 Phe Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
 65 70 75
 Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
 15 80 85 90
 Thr Tyr Tyr Cys Ser Gln Ser Thr His Val Pro Leu Thr Phe Gly
 95 100 105
 20 Gln Gly Thr Lys Val Glu Ile Lys Arg
 110 114

(2) INFORMATION FOR SEQ ID NO:47:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1 5 10 15
 35 Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Thr Ile Ser
 20 25 30
 Lys Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
 35 40 45
 40 Leu Leu Ile Tyr Tyr Ser Gly Ser Thr Leu Glu Ser Gly Val Pro
 50 55 60
 Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 45 65 70 75
 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
 80 85 90
 50 Gln His Asn Glu Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val
 95 100 105
 Glu Ile Lys Arg
 109

55

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

60

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

5	Glu	Ile	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Met	Lys	Pro	Gly	1	5	10	15
	Ala	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe	Ser	20	25	30	
10	Ser	His	Tyr	Met	His	Trp	Val	Lys	Gln	Ser	His	Gly	Lys	Ser	Leu	35	40	45	
	Glu	Trp	Ile	Gly	Tyr	Ile	Asp	Pro	Ser	Asn	Gly	Glu	Thr	Thr	Tyr	50	55	60	
15	Asn	Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Thr	Ser	65	70	75	
	Ser	Ser	Thr	Ala	Asn	Val	His	Leu	Ser	Ser	Leu	Thr	Ser	Asp	Asp	80	85	90	
20	Ser	Ala	Val	Tyr	Phe	Cys	Ala	Ala	Arg	Gly	Asp	Tyr	Arg	Tyr	Asn	95	100	105	
25	Gly	Asp	Trp	Phe	Phe	Asp	Val	Trp	Gly	Ala	Gly	Thr				110	115	117	

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

35	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	1	5	10	15
40	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Tyr	Ser	Phe	Ser	20	25	30	
	Ser	His	Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	35	40	45	
45	Glu	Trp	Val	Gly	Tyr	Ile	Asp	Pro	Ser	Asn	Gly	Glu	Thr	Thr	Tyr	50	55	60	
	Asn	Gln	Lys	Phe	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	65	70	75	
50	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	80	85	90	
55	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Arg	Gly	Asp	Tyr	Arg	Tyr	Asn	95	100	105	
	Gly	Asp	Trp	Phe	Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr				110	115	117	

60 (2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	
	1				5					10					15	
10	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Ser	Phe	Thr	
					20					25					30	
	Gly	His	Trp	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
					35					40					45	
15	Glu	Trp	Val	Gly	Met	Ile	His	Pro	Ser	Asp	Ser	Glu	Thr	Arg	Tyr	
					50					55					60	
	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	
20					65					70					75	
	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	
					80					85					90	
25	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Arg	Gly	Ile	Tyr	Phe	Tyr	Gly	
					95					100					105	
	Thr	Thr	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr					
					110					115	116					

30 (2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 242 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

40	Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	
	1				5					10					15	
	Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Asp	Ile	Gln	Met	Thr	Gln	Ser	
					20					25					30	
45	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	
					35					40					45	
	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Gly	Ile	Gly	Asn	Thr	Tyr	
50					50					55					60	
	Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	
					65					70					75	
55	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Ser	Arg	Phe	
					80					85					90	
	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	
					95					100					105	
60	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Ser	Gln	Ser	Thr	
					110					115					120	

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      His Val Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
                125                      130                      135
5    Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
                140                      145                      150
      Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
                155                      160                      165
10   Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
                170                      175                      180
      Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
15   185                      190                      195
      Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
                200                      205                      210
20   Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr
                215                      220                      225
      His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly
                230                      235                      240
25   Glu Cys
      242

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(2) INFORMATION FOR SEQ ID NO:52:

30

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 253 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
 1                5                10                15
40   Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Gln Ser
      20                25                30
45   Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
      35                40                45
      Ala Ala Ser Gly Tyr Ser Phe Ser Ser His Tyr Met His Trp Val
      50                55                60
50   Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Tyr Ile Asp
      65                70                75
      Pro Ser Asn Gly Glu Thr Thr Tyr Asn Gln Lys Phe Lys Gly Arg
      80                85                90
55   Phe Thr Leu Ser Arg Asp Asn Ser Lys Asn Thr Ala Tyr Leu Gln
      95                100               105
60   Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala
      110               115                120
      Arg Gly Asp Tyr Arg Tyr Asn Gly Asp Trp Phe Phe Asp Val Trp

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		125		130		135
	Gly Gln Gly Thr	Leu Val Thr Val Ser	Ser Ala Ser Thr Lys Gly			
		140	145		150	
5	Pro Ser Val Phe	Pro Leu Ala Pro Ser	Ser Lys Ser Thr Ser Gly			
		155	160		165	
	Gly Thr Ala Ala	Leu Gly Cys Leu Val	Lys Asp Tyr Phe Pro Glu			
10		170	175		180	
	Pro Val Thr Val	Ser Trp Asn Ser Gly	Ala Leu Thr Ser Gly Val			
		185	190		195	
15	His Thr Phe Pro	Ala Val Leu Gln Ser	Ser Gly Leu Tyr Ser Leu			
		200	205		210	
	Ser Ser Val Val	Thr Val Pro Ser Ser	Ser Leu Gly Thr Gln Thr			
20		215	220		225	
	Tyr Ile Cys Asn	Val Asn His Lys Pro	Ser Asn Thr Lys Val Asp			
		230	235		240	
25	Lys Lys Val Glu	Pro Lys Ser Cys Asp	Lys Thr His Thr			
		245	250		253	

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 159 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

35	Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met	
	1 5 10 15	
40	Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn	
	20 25 30	
	Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala Thr	
	35 40 45	
45	Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly	
	50 55 60	
	Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Ser	
50	65 70 75	
	Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu	
	80 85 90	
55	Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val	
	95 100 105	
	Glu Cys Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu Phe	
	110 115 120	
60	Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala	
	125 130 135	

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Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe
140 145 150

5 Ala Asn Ile Leu Arg Asn Lys Glu Ser
155 159

(2) INFORMATION FOR SEQ ID NO:54:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 780 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTTTCTAT 50
20 TGCTACAAAC GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC 100
TGTC CGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCAG GTCAAGTCAA 150
AGCTTAGTAC ATGGTATAGG TAACACGTAT TTACTCTGGT ATCAACAGAA 200
25 ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC AATCGATTCT 250
CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT 300
30 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC 350
ACAGAGTACT CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA 400
TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT 450
35 GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC TGAATAACTT 500
CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT 550
40 CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600
TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650
CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700
45 CAAAGAGCTT CAACAGGGGA GAGTGTTAAG CTGATCCTCT ACGCCGGACG 750
CATCGTGGCC CTAGTACGCA ACTAGTCGTA 780

50 (2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 amino acids
(B) TYPE: Amino Acid
55 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

60 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
1 5 10 15

Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser

	20	25	30
	Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys		
	35	40	45
5	Ala Ala Ser Gly Tyr Ser Phe Ser Ser His Tyr Met His Trp Val		
	50	55	60
10	Lys Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Tyr Ile Asp		
	65	70	75
	Pro Ser Asn Gly Glu Thr Thr Tyr Asn Gln Lys Phe Lys Gly Arg		
	80	85	90
15	Phe Thr Leu Ser Arg Asp Asn Ser Lys Asn Thr Ala Tyr Leu Gln		
	95	100	105
	Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala		
	110	115	120
20	Arg Gly Asp Tyr Arg Tyr Asn Gly Asp Trp Phe Phe Asp Val Trp		
	125	130	135
	Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly		
25	140	145	150
	Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly		
	155	160	165
30	Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu		
	170	175	180
	Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val		
	185	190	195
35	His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu		
	200	205	210
	Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr		
40	215	220	225
	Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp		
	230	235	240
45	Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr		
	245	250	253

(2) INFORMATION FOR SEQ ID NO:56:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 242 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear
- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe		
1	5	10
15		
60 Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Gln Met Thr Gln Ser		
20	25	30

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	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	
					35					40					45	
5	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Gly	Ile	Gly	Ala	Thr	Tyr	
					50					55					60	
	Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	
					65					70					75	
10	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Ser	Arg	Phe	
					80					85					90	
	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	
					95					100					105	
15	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Ser	Gln	Ser	Thr	
					110					115					120	
	His	Val	Pro	Leu	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	
20					125					130					135	
	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	
					140					145					150	
25	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	
					155					160					165	
	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	
					170					175					180	
30	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	
					185					190					195	
	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	
35					200					205					210	
	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	
					215					220					225	
40	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	
					230					235					240	
	Glu	Cys														
		242														

45

(2) INFORMATION FOR SEQ ID NO:57:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 45 amino acids
50	(B) TYPE: Amino Acid
	(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

55	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Arg	Met	Lys	
	1				5						10				15	
	Gln	Leu	Glu	Asp	Lys	Val	Glu	Glu	Leu	Leu	Ser	Lys	Asn	Tyr	His	
					20					25					30	
60	Leu	Glu	Asn	Glu	Val	Ala	Arg	Leu	Lys	Lys	Leu	Val	Gly	Glu	Arg	
					35					40					45	

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 5 (A) LENGTH: 780 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT 50
 15 TGCTACAAAC GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC 100
 TGTCCGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCAG GTCAAGTCAA 150
 20 AGCTTAGTAC ATGGTATAGG TGCTACGTAT TTACTCTGGT ATCAACAGAA 200
 ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC AATCGATTCT 250
 CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT 300
 25 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC 350
 ACAGAGTACT CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA 400
 TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT 450
 30 GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC TGAATAACTT 500
 CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT 550
 35 CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600
 TACAGCCTCA GCAGCACCCT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650
 CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700
 40 CAAAGAGCTT CAACAGGGGA GAGTGTAAAG CTGATCCTCT ACGCCGGACG 750
 CATCGTGGCC CTAGTACGCA ACTAGTCGTA 780

45 (2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 927 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

55 AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT 50
 TCTTCTTGCA TCTATGTTTCG TTTTCTCTAT TGCTACAAAC GCGTACGCTG 100
 60 AGGTTTCAGCT AGTGCAGTCT GGCGGTGGCC TGGTGCAGCC AGGGGGCTCA 150
 CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC TCCTTCTCGA GTCACTATAT 200

GCACTGGGTC CGTCAGGCCC CGGGTAAGGG CCTGGAATGG GTTGGATATA 250
 TTGATCCTTC CAATGGTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCGT 300
 5 TTCACCTTAT CTCGCGACAA CTCCAAAAAC ACAGCATACC TGCAGATGAA 350
 CAGCCTGCGT GCTGAGGACA CTGCCGTCTA TTACTGTGCA AGAGGGGATT 400
 10 ATCGCTACAA TGGTGACTGG TTCTTCGACG TCTGGGGTCA AGGAACCCTG 450
 GTCACCGTCT CCTCGGCCCTC CACCAAGGGC CCATCGGTCT TCCCCCTGGC 500
 ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG 550
 15 TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC 600
 CTGACCAGCG GCGTGACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT 650
 20 CTACTCCCTC AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC 700
 AGACCTACAT CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTCGAC 750
 AAGAAAGTTG AGCCCAAATC TTGTGACAAA ACTCACACAT GCCCGCCGTG 800
 25 CCCAGCACCA GAACTGCTGG GCGGCCGCAT GAAACAGCTA GAGGACAAGG 850
 TCGAAGAGCT ACTCTCCAAG AACTACCACC TAGAGAATGA AGTGGCAAGA 900
 30 CTCAAAAAGC TTGTCGGGGA GCGCTAA 927

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 298 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

40 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
 1 5 10 15
 Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Gln Ser
 45 20 25 30
 Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
 35 40 45
 50 Ala Ala Ser Gly Tyr Ser Phe Ser Ser His Tyr Met His Trp Val
 50 55 60
 Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Tyr Ile Asp
 65 70 75
 55 Pro Ser Asn Gly Glu Thr Thr Tyr Asn Gln Lys Phe Lys Gly Arg
 80 85 90
 Phe Thr Leu Ser Arg Asp Asn Ser Lys Asn Thr Ala Tyr Leu Gln
 60 95 100 105
 Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala

	110	115	120
	Arg Gly Asp Tyr	Arg Tyr Asn Gly Asp	Trp Phe Phe Asp Val Trp
	125	130	135
5	Gly Gln Gly Thr	Leu Val Thr Val Ser	Ser Ala Ser Thr Lys Gly
	140	145	150
10	Pro Ser Val Phe	Pro Leu Ala Pro Ser	Ser Lys Ser Thr Ser Gly
	155	160	165
	Gly Thr Ala Ala	Leu Gly Cys Leu Val	Lys Asp Tyr Phe Pro Glu
	170	175	180
15	Pro Val Thr Val	Ser Trp Asn Ser Gly	Ala Leu Thr Ser Gly Val
	185	190	195
	His Thr Phe Pro	Ala Val Leu Gln Ser	Ser Gly Leu Tyr Ser Leu
	200	205	210
20	Ser Ser Val Val	Thr Val Pro Ser Ser	Ser Leu Gly Thr Gln Thr
	215	220	225
	Tyr Ile Cys Asn	Val Asn His Lys Pro	Ser Asn Thr Lys Val Asp
	230	235	240
	Lys Lys Val Glu	Pro Lys Ser Cys Asp	Lys Thr His Thr Cys Pro
	245	250	255
30	Pro Cys Pro Ala	Pro Glu Leu Leu Gly	Gly Arg Met Lys Gln Leu
	260	265	270
	Glu Asp Lys Val	Glu Glu Leu Leu Ser	Lys Asn Tyr His Leu Glu
	275	280	285
35	Asn Glu Val Ala	Arg Leu Lys Lys Leu	Val Gly Glu Arg
	290	295	298

(2) INFORMATION FOR SEQ ID NO:61:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6563 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - 45 (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

50 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC 50

TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT 100

55 GAACTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT 150

TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG 200

GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCTGA CGACGATACG 250

60 GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA 300

AAAAGTTAAT CTTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT 350

ATAGTCGCTT TGTTTTTATT TTTTAATGTA TTTGTAACTA GAATTCGAGC 400
 TCGGTACCCG GGGATCCTCT CGAGGTTGAG GTGATTTTAT GAAAAAGAAT 450
 5 ATCGCATTTT TTCTTGCATC TATGTTTCGTT TTTTCTATTG CTACAAACGC 500
 ATACGCTGAT ATCCAGATGA CCCAGTCCCC GAGCTCCCTG TCCGCCTCTG 550
 10 TGGGCGATAG GGTCAACATC ACCTGCAGGT CAAGTCAAAG CTTAGTACAT 600
 GGTATAGGTG CTACGTATTT ACACTGGTAT CAACAGAAAC CAGGAAAAGC 650
 TCCGAAACTA CTGATTTACA AAGTATCCAA TCGATTCTCT GGAGTCCCTT 700
 15 CTCGCTTCTC TGGATCCGGT TCTGGGACGG ATTTCACTCT GACCATCAGC 750
 AGTCTGCAGC CAGAAGACTT CGCAACTTAT TACTGTTTAC AGAGTACTCA 800
 20 TGTCCCGCTC ACGTTTGGAC AGGGTACCAA GGTGGAGATC AAACGAACTG 850
 TGGCTGCACC ATCTGTCTTC ATCTTCCCGC CATCTGATGA GCAGTTGAAA 900
 TCTGGAAGTG CTTCTGTTGT GTGCCTGCTG AATAACTTCT ATCCCAGAGA 950
 25 GGCCAAAGTA CAGTGAAGG TGGATAACGC CCTCCAATCG GGTAAGTCCC 1000
 AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC 1050
 30 AGCACCTTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC 1100
 CTGCGAAGTC ACCCATCAGG GCCTGAGCTC GCCCGTCACA AAGAGCTTCA 1150
 ACAGGGGAGA GTGTTAAGCT GATCCTCTAC GCCGGACGCA TCGTGGCCCT 1200
 35 AGTACGCAAC TAGTCGTAAG AAGGGTATCT AGAGGTTGAG GTGATTTTAT 1250
 GAAAAAGAAT ATCGCATTTT TTCTTGCATC TATGTTTCGTT TTTTCTATTG 1300
 40 CTACAAACGC GTACGCTGAG GTTCAGCTAG TGCAGTCTGG CCGTGGCCTG 1350
 GTGCAGCCAG GGGGCTCACT CCGTTTGTCC TGTGCAGCTT CTGGCTACTC 1400
 CTTCTCGAGT CACTATATGC ACTGGGTCCG TCAGGCCCCG GGTAAGGGCC 1450
 45 TGAATGGGT TGGATATATT GATCCTTCCA ATGGTGAAAC TACGTATAAT 1500
 CAAAAGTTCA AGGGCCGTTT CACTTTATCT CGCGACAACT CCAAAAACAC 1550
 50 AGCATACCTG CAGATGAACA GCCTGCGTGC TGAGGACACT GCCGTCTATT 1600
 ACTGTGCAAG AGGGGATTAT CGCTACAATG GTGACTGGTT CTTGACGTC 1650
 TGGGGTCAAG GAACCCTGGT CACCGTCTCC TCGGCCTCCA CCAAGGGCCC 1700
 55 ATCGGTCTTC CCCCTGGCAC CCTCCTCCAA GAGCACCTCT GGGGGCACAG 1750
 CGGCCCTGGG CTGCCTGGTC AAGGACTACT TCCCCGAACC GGTGACGGTG 1800
 60 TCGTGGAAGT CAGGCGCCCT GACCAGCGGC GTGCACACCT TCCCGGCTGT 1850
 CCTACAGTCC TCAGGACTCT ACTCCCTCAG CAGCGTGGTG ACCGTGCCCT 1900

CCAGCAGCTT GGGCACCCAG ACCTACATCT GCAACGTGAA TCACAAGCCC 1950
 5 AGCAACACCA AGGTCGACAA GAAAGTTGAG CCCAAATCTT GTGACAAAAC 2000
 TCACACATGC CCGCCGTGCC CAGCACCAGA ACTGCTGGGC GGCCGCATGA 2050
 AACAGCTAGA GGACAAGGTC GAAGAGCTAC TCTCCAAGAA CTACCACCTA 2100
 10 GAGAATGAAG TGGCAAGACT CAAAAAGCTT GTCGGGGAGC GCTAAGCATG 2150
 CGACGGCCCT AGAGTCCCTA ACGCTCGGTT GCCGCCGGGC GTTTTTTATT 2200
 GTTAACTCAT GTTTGACAGC TTATCATCGA TAAGCTTTAA TGCGGTAGTT 2250
 15 TATCACAGTT AAATTGCTAA CGCAGTCAGG CACCGTGTAT GAAATCTAAC 2300
 AATGCGCTCA TCGTCATCCT CGGCACCGTC ACCCTGGATG CTGTAGGCAT 2350
 20 AGGCTTGGTT ATGCCGGTAC TGCCGGGCCT CTTGCGGGAT ATCGTCCATT 2400
 CCGACAGCAT CGCCAGTCAC TATGGCGTGC TGCTAGCGCT ATATGCGTTG 2450
 ATGCAATTTT TATGCGCACC CGTTCTCGGA GCACTGTCCG ACCGCTTTGG 2500
 25 CCGCCGCCCA GTCCTGCTCG CTTGCTACT TGGAGCCACT ATCGACTACG 2550
 CGATCATGGC GACCACACCC GTCCTGTGGA TCCTCTACGC CGGACGCATC 2600
 30 GTGGCCGGCA TCACCGGCGC CACAGGTGCG GTTGCTGGCG CCTATATCGC 2650
 CGACATCACC GATGGGGAAG ATCGGGCTCG CCACTTCGGG CTCATGAGCG 2700
 CTTGTTTCGG CGTGGGTATG GTGGCAGGCC CCGTGGCCGG GGGACTGTTG 2750
 35 GGCGCCATCT CTTGACGCG ACCATTCCCTT GCGGCGGCGG TGCTCAACGG 2800
 CCTCAACCTA CTACTGGGCT GCTTCCTAAT GCAGGAGTCG CATAAGGGAG 2850
 40 AGCGTCGTCC GATGCCCTTG AGAGCCTTCA ACCCAGTCAG CTCCTTCCGG 2900
 TGGGCGCGGG GCATGACTAT CGTCGCCGCA CTTATGACTG TCTTCTTTAT 2950
 CATGCAACTC GTAGGACAGG TGCCGGCAGC GCTCTGGGTC ATTTTCGGCG 3000
 45 AGGACCGCTT TCGCTGGAGC GCGACGATGA TCGGCCTGTC GCTTGCGGTA 3050
 TTCGGAATCT TGCACGCCCT CGCTCAAGCC TTCGTCAGTG GTCCCGCCAC 3100
 50 CAAACGTTTC GGCGAGAAGC AGGCCATTAT CGCCGGCATG GCGGCCGACG 3150
 CGCTGGGCTA CGTCTTGCTG GCGTTCGCGA CGCGAGGCTG GATGGCCTTC 3200
 CCCATTATGA TTCTTCTCGC TTCCGGCGGC ATCGGGATGC CCGCGTTGCA 3250
 55 GGCCATGCTG TCCAGGACAGG TAGATGACGA CCATCAGGGA CAGCTTCAAG 3300
 GATCGCTCGC GGCTCTTACC AGCCTAACTT CGATCACTGG ACCGCTGATC 3350
 60 GTCACGGCGA TTTATGCCGC CTCGGCGAGC ACATGGAACG GGTTGGCATG 3400
 GATTGTAGGC GCCGCCCTAT ACCTTGTCTG CCTCCCCGCG TTGCGTCGCG 3450

GTGCATGGAG CCGGGCCACC TCGACCTGAA TGGAAGCCGG CGGCACCTCG 3500
 CTAACGGATT CACCACTCCA AGAATTGGAG CCAATCAATT CTTGCGGAGA 3550
 5 ACTGTGAATG CGCAAACCAA CCCTTGGCAG AACATATCCA TCGCGTCCGC 3600
 CATCTCCAGC AGCCGCACGC GGCATCTC GGCAGCGTT GGGTCCTGGC 3650
 10 CACGGGTGCG CATGATCGTG CTCCTGTCGT TGAGGACCCG GCTAGGCTGG 3700
 CGGGGTGCG TTACTGGTTA GCAGAATGAA TCACCGATAC GCGAGCGAAC 3750
 GTGAAGCGAC TGCTGCTGCA AAACGTCTGC GACCTGAGCA ACAACATGAA 3800
 15 TGGTCTTCGG TTTCCGTGTT TCGTAAAGTC TGGAAACGCG GAAGTCAGCG 3850
 CCCTGCACCA TTATGTTCCG GATCTGCATC GCAGGATGCT GCTGGCTACC 3900
 20 CTGTGGAACA CCTACATCTG TATTAACGAA GCGCTGGCAT TGACCCTGAG 3950
 TGATTTTCT CTGGTCCCGC CGCATCCATA CCGCCAGTTG TTTACCCTCA 4000
 CAACGTTCCA GTAACCGGGC ATGTTTCATCA TCAGTAACCC GTATCGTGAG 4050
 25 CATCCTCTCT CGTTTCATCG GTATCATTAC CCCCATGAAC AGAAATTCCC 4100
 CCTTACACGG AGGCATCAAG TGACCAAACA GGAAAAAACC GCCCTTAACA 4150
 30 TGGCCCGCTT TATCAGAAGC CAGACATTAA CGCTTCTGGA GAAACTCAAC 4200
 GAGCTGGACG CGGATGAACA GGCAGACATC TGTGAATCGC TTCACGACCA 4250
 CGCTGATGAG CTTTACCGCA GCTGCCTCGC GCGTTTCGGT GATGACGGTG 4300
 35 AAAACCTCTG ACACATGCAG CTCCCGGAGA CGGTCACAGC TTGTCTGTAA 4350
 GCGGATGCCG GGAGCAGACA AGCCCGTCAG GCGCGTCAG CGGGTGTTGG 4400
 40 CGGGTGTCGG GCGCAGCCA TGACCCAGTC ACGTAGCGAT AGCGGAGTGT 4450
 ATACTGGCTT AACTATGCGG CATCAGAGCA GATTGTACTG AGAGTGCACC 4500
 ATATGCGGTG TGAAATACCG CACAGATGCG TAAGGAGAAA ATACCGCATC 4550
 45 AGGCGCTCTT CCGCTCCTC GCTCACTGAC TCGCTGCGCT CGGTGCTTCG 4600
 GCTGCGGCGA GCGGTATCAG CTCCTCAAA GCGGTAATA CGGTTATCCA 4650
 50 CAGAATCAGG GGATAACGCA GGAAAGAACA TGTGAGCAA AGGCCAGCAA 4700
 AAGGCCAGGA ACCGTAAAAA GGCCGCGTTG CTGGCGTTTT TCCATAGGCT 4750
 CCGCCCCCT GACGAGCATC AAAAAATCG ACGCTCAAGT CAGAGGTGGC 4800
 55 GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC TGGAAGCTCC 4850
 CTCGTGCGCT CTCCTGTTCC GACCCTGCCG CTTACCGGAT ACCTGTCCGC 4900
 60 CTTTCTCCCT TCGGGAAGCG TGGCGCTTTC TCATAGCTCA CGCTGTAGGT 4950
 ATCTCAGTTC GGTGTAGGTC GTTCGCTCCA AGCTGGGCTG TGTGCACGAA 5000

CCCCCGTTT AGCCCGACCG CTGCGCCTTA TCCGGTAACT ATCGTCTTGA 5050
 GTCCAACCCG GTAAGACACG ACTTATCGCC ACTGGCAGCA GCCACTGGTA 5100
 5 ACAGGATTAG CAGAGCGAGG TATGTAGGCG GTGCTACAGA GTTCTTGAAG 5150
 TGGTGGCCTA ACTACGGCTA CACTAGAAGG ACAGTATTTG GTATCTGCGC 5200
 10 TCTGCTGAAG CCAGTTACCT TCGGAAAAAG AGTTGGTAGC TCTTGATCCG 5250
 GCAAACAAAC CACCGCTGGT AGCGGTGGTT TTTTGTGTTG CAAGCAGCAG 5300
 ATTACGCGCA GAAAAAAGG ATCTCAAGAA GATCCTTTGA TCTTTTCTAC 5350
 15 GGGGTCTGAC GCTCAGTGGA ACGAAAACTC ACGTTAAGGG ATTTTGGTCA 5400
 TGAGATTATC AAAAAGGATC TTCACCTAGA TCCTTTTAAA TTAAAAATGA 5450
 20 AGTTTTTAAAT CAATCTAAAG TATATATGAG TAAACTTGGT CTGACAGTTA 5500
 CCAATGCTTA ATCAGTGAGG CACCTATCTC AGCGATCTGT CTATTTTCGTT 5550
 CATCCATAGT TGCCTGACTC CCCGTCGTGT AGATAACTAC GATACGGGAG 5600
 25 GGCTTACCAT CTGGCCCCAG TGCTGCAATG ATACCGCGAG ACCCACGCTC 5650
 ACCGGCTCCA GATTTATCAG CAATAAACCA GCCAGCCGGA AGGGCCGAGC 5700
 30 GCAGAAAGTG TCCTGCAACT TTATCCGCCT CCATCCAGTC TATTAATTGT 5750
 TGCCGGGAAG CTAGAGTAAG TAGTTCGCCA GTTAATAGTT TGCGCAACGT 5800
 TGTTGCCATT GCTGCAGGCA TCGTGGTGTC ACGCTCGTCG TTTGGTATGG 5850
 35 CTTCAATCAG CTCCGGTTCC CAACGATCAA GGCGAGTTAC ATGATCCCCC 5900
 ATGTTGTGCA AAAAAGCGGT TAGCTCCTTC GGTCTCCGA TCGTTGTCAG 5950
 40 AAGTAAGTTG GCCGCAGTGT TATCACTCAT GGTTATGGCA GCACTGCATA 6000
 ATTCTCTTAC TGTCATGCCA TCCGTAAGAT GCTTTTCTGT GACTGGTGAG 6050
 TACTCAACCA AGTCATTCTG AGAATAGTGT ATGCGGCGAC CGAGTTGCTC 6100
 45 TTGCCCCGCG TCAACACGGG ATAATACCGC GCCACATAGC AGAACTTTAA 6150
 AAGTGCTCAT CATTGGAAAA CGTTCTTCGG GGCGAAAACT CTCAAGGATC 6200
 50 TTACCGCTGT TGAGATCCAG TTCGATGTAA CCCACTCGTG CACCCAACTG 6250
 ATCTTCAGCA TCTTTTACTT TCACCAGCGT TTCTGGGTGA GCAAAAACAG 6300
 GAAGGCAAAA TGCCGCAAAA AAGGGAATAA GGGCGACACG GAAATGTTGA 6350
 55 ATACTCATAC TCTTCCTTTT TCAATATTAT TGAAGCATTT ATCAGGGTTA 6400
 TTGTCTCATG AGCGGATACA TATTTGAATG TATTTAGAAA AATAAACAAA 6450
 60 TAGGGGTTC GCGCACATTT CCCCAGAAAAG TGCCACCTGA CGTCTAAGAA 6500
 ACCATTATTA TCATGACATT AACCTATAAA AATAGGCGTA TCACGAGGCC 6550

CTTTCGTCTT CAA 6563

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 242 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	1	5	10	15
Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Asp	Ile	Gln	Met	Thr	Gln	Ser	20	25	30	
Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	35	40	45	
Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Gly	Ile	Gly	Glu	Thr	Tyr	50	55	60	
Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	65	70	75	
Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Ser	Arg	Phe	80	85	90	
Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	95	100	105	
Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Ser	Gln	Ser	Thr	110	115	120	
His	Val	Pro	Leu	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	125	130	135	
Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	140	145	150	
Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	155	160	165	
Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	170	175	180	
Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	185	190	195	
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	200	205	210	
Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	215	220	225	
His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	230	235	240	
Glu	Cys														242			

(2) INFORMATION FOR SEQ ID NO:63:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CATGGTATAG GTTAAACTTA TTTACAC 27

15 (2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: Nucleic Acid
 20 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

25 CATGGTATAG GTNNSACTTA TTTACAC 27

(2) INFORMATION FOR SEQ ID NO:65:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 780 base pairs
 (B) TYPE: Nucleic Acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTTTCTAT 50
 40 TGCTACAAAC GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC 100
 TGTCCGCCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCAG GTCAAGTCAA 150
 45 AGCTTAGTAC ATGGTATAGG TGAGACGTAT TTACACTGGT ATCAACAGAA 200
 ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC AATCGATTCT 250
 CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT 300
 50 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC 350
 ACAGAGTACT CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA 400
 55 TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT 450
 GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC TGAATAACTT 500
 CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT 550
 60 CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600

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TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650
CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700
5 CAAAGAGCTT CAACAGGGGA GAGTGTTAAG CTGATCCTCT ACGCCGGACG 750
CATCGTGGCC CTAGTACGCA ACTAGTCGTA 780

(2) INFORMATION FOR SEQ ID NO:66:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

20

CTAGTGCAGT CTGGCGGTGG CCTGGTGCAG CCAGGGGGCT CACTCCGTTT 50

GTCCTGTGCA GCTTCTGGCT ACTCCTTC 78

(2) INFORMATION FOR SEQ ID NO:67:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

30

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

35

TCGAGAAGGA GTAGCCAGAA GCTGCACAGG ACAAACGGAG TGAGCCCCCT 50

GGCTGCACCA GGCCACCGCC AGACTGCACT AG 82

(2) INFORMATION FOR SEQ ID NO:68:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8120 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

45

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

50

TTCGAGCTCG CCCGACATTG ATTATTGACT AGAGTCGATC GACAGCTGTG 50

GAATGTGTGT CAGTTAGGGT GTGGAAAGTC CCCAGGCTCC CCAGCAGGCA 100

GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAG GTGTGGAAAG 150

55

TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC ATCTCAATTA 200

GTCAGCAACC ATAGTCCCGC CCCTAACTCC GCCCATCCCG CCCCTAACTC 250

60

CGCCCAGTTC CGCCCATTCT CCGCCCCATG GCTGACTAAT TTTTTTTATT 300

TATGCAGAGG CCGAGGCCGC CTCGGCCTCT GAGCTATTCC AGAAGTAGTG 350

AGGAGGCTTT TTTGGAGGCC TAGGCTTTTG CAAAAAGCTA GCTTATCCGG 400
 CCGGGAACGG TGCATTGGAA CGCGGATTCC CCGTGCCAAG AGTGACGTAA 450
 5 GTACCGCCTA TAGAGCGATA AGAGGATTTT ATCCCCGCTG CCATCATGGT 500
 TCGACCATTG AACTGCATCG TCGCCGTGTC CCAAAATATG GGGATTGGCA 550
 10 AGAACGGAGA CCTACCCTGG CCTCCGCTCA GGAACGAGTT CAAGTACTTC 600
 CAAAGAATGA CCACAACCTC TTCAGTGGAA GGTAAACAGA ATCTGGTGAT 650
 TATGGGTAGG AAAACCTGGT TCTCCATTCC TGAGAAGAAT CGACCTTTAA 700
 15 AGGACAGAAT TAATATAGTT CTCAGTAGAG AACTCAAAGA ACCACCACGA 750
 GGAGCTCATT TTCTTGCCAA AAGTTTGGAT GATGCCTTAA GACTTATTGA 800
 20 ACAACCGGAA TTGGCAAGTA AAGTAGACAT GGTTTGGATA GTCGGAGGCA 850
 GTTCTGTTTA CCAGGAAGCC ATGAATCAAC CAGGCCACCT TAGACTCTTT 900
 GTGACAAGGA TCATGCAGGA ATTTGAAAGT GACACGTTTT TCCAGAAAT 950
 25 TGATTTGGGG AAATATAAAC CTCTCCCAGA ATACCCAGGC GTCCTCTCTG 1000
 AGGTCCAGGA GGAAAAAGGC ATCAAGTATA AGTTTGAAGT CTACGAGAAG 1050
 30 AAAGACTAAC AGGAAGATGC TTTCAAGTTC TCTGCTCCCC TCCTAAAGCT 1100
 ATGCATTTTT ATAAGACCAT GGGACTTTTG CTGGCTTTAG ATCCCCTTGG 1150
 CTTCGTTAGA ACGCAGCTAC AATTAATACA TAACCTTATG TATCATAAC 1200
 35 ATACGATTTA GGTGACACTA TAGATAACAT CCACTTTGCC TTTCTCTCCA 1250
 CAGGTGTCCA CTCCCAGGTC CAACTGCACC TCGGTTCTAT CGATTGAATT 1300
 40 CCACCATGGG ATGGTCATGT ATCATCCTTT TTCTAGTAGC AACTGCAACT 1350
 GGAGTACATT CAGAAGTTCA GCTAGTGCAG TCTGGCGGTG GCCTGGTGCA 1400
 GCCAGGGGGC TCACTCCGTT TGTCTGTGC AGCTTCTGGC TACTCCTTCT 1450
 45 CGAGTCACTA TATGCACTGG GTCCGTCAGG CCCCGGGTAA GGGCCTGGAA 1500
 TGGGTTGGAT ATATTGATCC TTCCAATGGT GAAACTACGT ATAATCAAAA 1550
 50 GTTCAAGGGC CGTTTCACTT TATCTCGCGA CAACTCCAAA AACACAGCAT 1600
 ACCTGCAGAT GAACAGCCTG CGTGCTGAGG AACTGCCGT CTATTACTGT 1650
 GCAAGAGGGG ATTATCGCTA CAATGGTGAC TGGTTCTTCG ACGTCTGGGG 1700
 55 TCAAGGAACC CTGGTCACCG TCTCCTCGGC CTCCACCAAG GGCCCATCGG 1750
 TCTTCCCCCT GGCACCCTCC TCCAAGAGCA CCTCTGGGGG CACAGCGGCC 1800
 60 CTGGGCTGCC TGGTCAAGGA CTACTTCCCC GAACCGGTGA CGGTGTCGTG 1850
 GAACTCAGGC GCCCTGACCA GCGGCGTGCA CACCTTCCCG GCTGTCCTAC 1900

AGTCCTCAGG ACTCTACTCC CTCAGCAGCG TGGTGACTGT GCCCTCTAGC 1950
 AGCTTGGGCA CCCAGACCTA CATCTGCAAC GTGAATCACA AGCCCAGCAA 2000
 5 CACCAAGGTG GACAAGAAAG TTGAGCCCAA ATCTTGTGAC AAAACTCACA 2050
 CATGCCCACC GTGCCCAGCA CCTGAACTCC TGGGGGGACC GTCAGTCTTC 2100
 10 CTCTTCCCCC CAAAACCCAA GGACACCCTC ATGATCTCCC GGACCCCTGA 2150
 GGTACATGTC GTGGTGGTGG ACGTGAGCCA CGAAGACCCT GAGGTCAAGT 2200
 TCAACTGGTA CGTGGACGGC GTGGAGGTGC ATAATGCCAA GACAAAGCCG 2250
 15 CGGGAGGAGC AGTACAACAG CACGTACCGT GTGGTCAGCG TCCTCACCCT 2300
 CCTGCACCAG GACTGGCTGA ATGGCAAGGA GTACAAGTGC AAGGTCTCCA 2350
 20 ACAAAGCCCT CCCAGCCCCC ATCGAGAAAA CCATCTCCAA AGCCAAAGGG 2400
 CAGCCCCGAG AACCACAGGT GTACACCCTG CCCCCATCCC GGGAAAGAGAT 2450
 GACCAAGAAC CAGGTCAGCC TGACCTGCCT GGTCAAAGGC TTCTATCCCA 2500
 25 GCGACATCGC CGTGGAGTGG GAGAGCAATG GGCAGCCGGA GAACAACCTAC 2550
 AAGACCACGC CTCCCGTGCT GGACTCCGAC GGCTCCTTCT TCCTCTACAG 2600
 30 CAAGCTCACC GTGGACAAGA GCAGGTGGCA GCAGGGGAAC GTCTTCTCAT 2650
 GCTCCGTGAT GCATGAGGCT CTGCACAACC ACTACACGCA GAAGAGCCTC 2700
 TCCCTGTCTC CGGGTAAATG AGTGCGACGG CCCTAGAGTC GACCTGCAGA 2750
 35 AGCTTGGCCG CCATGGCCCA ACTTGTTTAT TGCAGCTTAT AATGGTTACA 2800
 AATAAGCAA TAGCATCACA AATTTACAA ATAAAGCATT TTTTCTACTG 2850
 40 CATTCTAGTT GTGGTTTGTC CAAACTCATC AATGTATCTT ATCATGTCTG 2900
 GATCGATCGG GAATTAATTC GGCGCAGCAC CATGGCCTGA AATAACCTCT 2950
 GAAAGAGGAA CTTGGTTAGG TACCTTCTGA GGCGGAAAGA ACCATCTGTG 3000
 45 GAATGTGTGT CAGTTAGGGT GTGGAAAGTC CCCAGGCTCC CCAGCAGGCA 3050
 GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAG GTGTGGAAAAG 3100
 50 TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC ATCTCAATTA 3150
 GTCAGCAACC ATAGTCCCGC CCCTAACTCC GCCCATCCCG CCCCTAACTC 3200
 CGCCAGTTTC CGCCCATTTCT CCGCCCCATG GCTGACTAAT TTTTTTTATT 3250
 55 TATGCAGAGG CCGAGGCCGC CTCGGCCTCT GAGCTATTCC AGAAGTAGTG 3300
 AGGAGGCTTT TTTGGAGGCC TAGGCTTTTG CAAAAGCTA GCTTATCCGG 3350
 60 CCGGGAACGG TGCATTGGAA CGCGGATTCC CCGTGCCAAG AGTCAGGTAA 3400
 GTACCGCCTA TAGAGTCTAT AGGCCACCC CTTGGCTTC GTTAGAACGC 3450

GGCTACAATT AATACATAAC CTTTTGGATC GATCCTACTG ACACTGACAT 3500
 5 CCACTTTTTTC TTTTCTCCA CAGGTGTCCA CTCCCAGGTC CAACTGCACC 3550
 TCGGTTTCGCG AAGCTAGCTT GGGCTGCATC GATTGAATTC CACCATGGGA 3600
 TGGTCATGTA TCATCCTTTT TCTAGTAGCA ACTGCAACTG GAGTACATTC 3650
 10 AGATATCCAG ATGACCCAGT CCCCAGGCTC CCTGTCCGCC TCTGTGGGCG 3700
 ATAGGGTCAC CATCACCTGC AGGTCAAGTC AAAGCTTAGT ACATGGTATA 3750
 GGTGCTACGT ATTTACTACTG GTATCAACAG AAACCAGGAA AAGCTCCGAA 3800
 15 ACTACTGATT TACAAAGTAT CCAATCGATT CTCTGGAGTC CCTTCTCGCT 3850
 TCTCTGGATC CGGTTCTGGG ACGGATTTCA CTCTGACCAT CAGCAGTCTG 3900
 20 CAGCCAGAAG ACTTCGCAAC TTATTACTGT TCACAGAGTA CTCATGTCCC 3950
 GCTCACGTTT GGACAGGGTA CCAAGGTGGA GATCAAACGA ACTGTGGCTG 4000
 CACCATCTGT CTTTCATCTTC CCGCCATCTG ATGAGCAGTT GAAATCTGGA 4050
 25 ACTGCTTCTG TTGTGTGCCT GCTGAATAAC TTCTATCCCA GAGAGGCCAA 4100
 AGTACAGTGG AAGGTGGATA ACGCCCTCCA ATCGGGTAAC TCCCAGGAGA 4150
 30 GTGTCACAGA GCAGGACAGC AAGGACAGCA CCTACAGCCT CAGCAGCACC 4200
 CTGACGCTGA GCAAAGCAGA CTACGAGAAA CACAAAGTCT ACGCCTGCGA 4250
 AGTCACCCAT CAGGGCCTGA GCTCGCCCGT CACAAAGAGC TTCAACAGGG 4300
 35 GAGAGTGTTA AGCTTGGCCG CCATGGCCCA ACTTGTTTAT TGCAGCTTAT 4350
 AATGGTTACA AATAAAGCAA TAGCATCACA AATTTACAA ATAAAGCATT 4400
 40 TTTTTCCTG CATTCTAGTT GTGGTTTGTC CAAACTCATC AATGTATCTT 4450
 ATCATGTCTG GATCGATCGG GAATTAATTC GGCGCAGCAC CATGGCCTGA 4500
 AATAACCTCT GAAAGAGGAA CTTGGTTAGG TACCTTCTGA GGCGGAAAGA 4550
 45 ACCAGCTGTG GAATGTGTGT CAGTTAGGGT GTGGAAAGTC CCCAGGCTCC 4600
 CCAGCAGGCA GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAG 4650
 50 GTGTGGAAAG TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC 4700
 ATCTCAATTA GTCAGCAACC ATAGTCCCGC CCCTAACTCC GCCCATCCCG 4750
 CCCCTAACTC CGCCCAGTTC CGCCCATCT CCGCCCCATG GCTGACTAAT 4800
 55 TTTTTTTATT TATGCAGAGG CCGAGGCCGC CTCGGCCTCT GAGCTATTCC 4850
 AGAAGTAGTG AGGAGGCTTT TTTGGAGGCC TAGGCTTTTG CAAAAGCTG 4900
 60 TTACCTCGAG CGGCCGCTTA ATTAAGGCGC GCCATTTAAA TCCTGCAGGT 4950
 AACAGCTTGG CACTGGCCGT CGTTTTACAA CGTCGTGACT GGGAAAACCC 5000

TGGCGTTACC CAACTTAATC GCCTTGCAGC ACATCCCCC TTCGCCAGCT 5050
 5 GGC GTAATAG CGAAGAGGCC CGCACCGATC GCCCTTCCCA ACAGTTGCGT 5100
 AGCCTGAATG GCGAATGGCG CCTGATGCGG TATTTTCTCC TTACGCATCT 5150
 GTGCGGTATT TCACACCGCA TACGTCAAAG CAACCATAGT ACGCGCCCTG 5200
 10 TAGCGGCGCA TTAAGCGCGG CGGGTGTGGT GGTACGCGC AGCGTGACCG 5250
 CTACACTTGC CAGCGCCCTA GCGCCCGCTC CTTTCGCTTT CTTCCCTTCC 5300
 TTTCTCGCCA CGTTCGCCCG CTTTCCCCGT CAAGCTCTAA ATCGGGGGCT 5350
 15 CCCTTTAGGG TTCCGATTTA GTGCTTTACG GCACCTCGAC CCCAAAAAAC 5400
 TTGATTTGGG TGATGGTTCA CGTAGTGGGC CATCGCCCTG ATAGACGGTT 5450
 20 TTTCGCCCTT TGACGTTGGA GTCCACGTTT TTTAATAGTG GACTCTTGTT 5500
 CCAAACCTGA ACAACACTCA ACCCTATCTC GGGCTATTCT TTTGATTTAT 5550
 AAGGGATTTT GCCGATTTTC GCCTATTGGT TAAAAAATGA GCTGATTTAA 5600
 25 CAAAAATTTA ACGCGAATTT TAACAAAATA TTAACGTTTA CAATTTTATG 5650
 GTGCACTCTC AGTACAATCT GCTCTGATGC CGCATAGTTA AGCCAACTCC 5700
 30 GCTATCGCTA CGTGACTGGG TCATGGCTGC GCCCCGACAC CCGCCAACAC 5750
 CCGCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGGCATC CGCTTACAGA 5800
 CAAGCTGTGA CCGTCTCCGG GAGCTGCATG TGTCAGAGGT TTTCACCGTC 5850
 35 ATCACCGAAA CGCGCGAGGC AGTATTCTTG AAGACGAAAG GGCCTCGTGA 5900
 TACGCCTATT TTTATAGGTT AATGTCATGA TAATAATGGT TTCTTAGACG 5950
 40 TCAGGTGGCA CTTTTCGGGG AAATGTGCGC GGAACCCCTA TTTGTTTATT 6000
 TTTCTAAATA CATTCAAATA TGTATCCGCT CATGAGACAA TAACCCTGAT 6050
 AAATGCTTCA ATAATATTGA AAAAGGAAGA GTATGAGTAT TCAACATTTT 6100
 45 CGTGTCGCCC TTATTCCCTT TTTTGCGGCA TTTTGCCTTC CTGTTTTTGC 6150
 TCACCCAGAA ACGCTGGTGA AAGTAAAAGA TGCTGAAGAT CAGTTGGGTG 6200
 50 CACGAGTGGG TTACATCGAA CTGGATCTCA ACAGCGGTAA GATCCTTGAG 6250
 AGTTTTTCGCC CCGAAGAACG TTTTCCAATG ATGAGCACTT TTAAAGTTCT 6300
 GCTATGTGGC GCGGTATTAT CCCGTGATGA CGCCGGGCAA GAGCAACTCG 6350
 55 GTCGCCGCAT ACACTATTCT CAGAATGACT TGGTTGAGTA CTCACCAGTC 6400
 ACAGAAAAGC ATCTTACGGA TGGCATGACA GTAAGAGAAT TATGCAGTGC 6450
 60 TGCCATAACC ATGAGTGATA AACTGCGGC CAACTTACTT CTGACAACGA 6500
 TCGGAGGACC GAAGGAGCTA ACCGCTTTTT TGCACAACAT GGGGGATCAT 6550

5 GTAACTCGCC TTGATCGTTG GGAACCGGAG CTGAATGAAG CCATACCAAA 6600
 CGACGAGCGT GACACCACGA TGCCAGCAGC AATGGCAACA ACGTTGCGCA 6650
 AACTATTAAC TGGCGAACTA CTTACTCTAG CTTCCCGGCA ACAATTAATA 6700
 GACTGGATGG AGGCGGATAA AGTTGCAGGA CCACTTCTGC GCTCGGCCCT 6750
 10 TCCGGCTGGC TGGTTTATTG CTGATAAATC TGGAGCCGGT GAGCGTGGGT 6800
 CTCGCGGTAT CATTCAGCA CTGGGGCCAG ATGGTAAGCC CTCCCGTATC 6850
 GTAGTTATCT ACACGACGGG GAGTCAGGCA ACTATGGATG AACGAAATAG 6900
 15 ACAGATCGCT GAGATAGGTG CCTCACTGAT TAAGCATTGG TAACTGTCAG 6950
 ACCAAGTTTA CTCATATATA CTTTAGATTG ATTTAAAACT TCATTTTTTAA 7000
 20 TTTAAAAGGA TCTAGGTGAA GATCCTTTTT GATAATCTCA TGACCAAAAT 7050
 CCCTTAACGT GAGTTTTTCGT TCCACTGAGC GTCAGACCCC GTAGAAAAGA 7100
 TCAAAGGATC TTCTTGAGAT CCTTTTTTTC TGCGCGTAAT CTGCTGCTTG 7150
 25 CAAACAAAAA AACCACCGCT ACCAGCGGTG GTTTGTGTTGC CGGATCAAGA 7200
 GCTACCAACT CTTTTTCCGA AGGTAAGTGG CTTTCAAGCA GCGCAGATAC 7250
 30 CAAATACTGT CCTTCTAGTG TAGCCGTAGT TAGGCCACCA CTTCAAGAAC 7300
 TCTGTAGCAC CGCCTACATA CCTCGCTCTG CTAATCCTGT TACCAGTGGC 7350
 TGCTGCCAGT GGCATAAGT CGTGTCTTAC CGGGTTGGAC TCAAGACGAT 7400
 35 AGTTACCGGA TAAGGCGCAG CGGTCGGGCT GAACGGGGGG TTCGTGCACA 7450
 CAGCCCAGCT TGGAGCGAAC GACCTACACC GAACTGAGAT ACCTACAGCG 7500
 40 TGAGCATTGA GAAAGCGCCA CGCTTCCCGA AGGGAGAAAG GCGGACAGGT 7550
 ATCCGGTAAG CGGCAGGGTC GGAACAGGAG AGCGCACGAG GGAGCTTCCA 7600
 GGGGGAAACG CCTGGTATCT TTATAGTCCT GTCGGGTTTC GCCACCTCTG 7650
 45 ACTTGAGCGT CGATTTTTGT GATGCTCGTC AGGGGGGCGG AGCCTATGGA 7700
 AAAACGCCAG CAACGCGGCC TTTTACGGT TCCTGGCCTT TTGCTGGCCT 7750
 50 TTTGCTCACA TGTCTTTTCC TGCATTATCC CCTGATTCTG TGGATAACCG 7800
 TATTACCGCC TTTGAGTGAG CTGATACCGC TCGCCGACAG CGAACGACCG 7850
 AGCGCAGCGA GTCAGTGAGC GAGGAAGCGG AAGAGCGCCC AATACGCAAA 7900
 55 CCGCCTCTCC CCGCGCGTTG GCCGATTAT TAATCCAGCT GGCACGACAG 7950
 GTTTCCCGAC TGGAAAGCGG GCAGTGAGCG CAACGCAATT AATGTGAGTT 8000
 60 ACCTCACTCA TTAGGCACCC CAGGCTTTAC ACTTTATGCT TCCGGCTCGT 8050
 ATGTTGTGTG GAATTGTGAG CGGATAACAA TTTCACACAG GAAACAGCTA 8100

TGACCATGAT TACGAATTAA 8120

(2) INFORMATION FOR SEQ ID NO:69:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 800 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

15 AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT 50
 TCTTCTTGCA TCTATGTTCTG TTTTCTCTAT TGCTACAAAC GCGTACGCTG 100
 AGGTTTCAGCT AGTGCAGTCT GGCAGTGGCC TGGTGCAGCC AGGGGGCTCA 150
 20 CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC TCCTTCTCGA GTCACATATAT 200
 GCACTGGGTC CGTCAGGCCC CGGGTAAGGG CCTGGAATGG GTTGGATATA 250
 25 TTGATCCTTC CAATGGTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCGT 300
 TTCACCTTTAT CTCGCGACAA CTCCAAAAAC ACAGCATACC TGCAGATGAA 350
 CAGCCTGCGT GCTGAGGACA CTGCCGTCTA TTA CTGTGCA AGAGGGGATT 400
 30 ATCGCTACAA TGGTGACTGG TTCTTCGACG TCTGGGGTCA AGGAACCCTG 450
 GTCACCGTCT CCTCGGCCTC CACCAAGGGC CCATCGGTCT TCCCCCTGGC 500
 35 ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG 550
 TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC 600
 CTGACCAGCG GCGTGACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT 650
 40 CTACTCCCTC AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC 700
 AGACCTACAT CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTCGAC 750
 45 AAGAAAGTTG AGCCCAAATC TTGTGACAAA ACTCACACAT GCCCGCCTGA 800

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 256 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

55

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe
 1 5 10 15
 Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Gln Ser
 60 20 25 30
 Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys

	35	40	45
	Ala Ala Ser Gly Tyr Ser Phe Ser Ser His Tyr Met His Trp Val		
	50	55	60
5	Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Tyr Ile Asp		
	65	70	75
	Pro Ser Asn Gly Glu Thr Thr Tyr Asn Gln Lys Phe Lys Gly Arg		
10	80	85	90
	Phe Thr Leu Ser Arg Asp Asn Ser Lys Asn Thr Ala Tyr Leu Gln		
	95	100	105
15	Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala		
	110	115	120
	Arg Gly Asp Tyr Arg Tyr Asn Gly Asp Trp Phe Phe Asp Val Trp		
20	125	130	135
	Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly		
	140	145	150
	Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly		
25	155	160	165
	Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu		
	170	175	180
30	Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val		
	185	190	195
	His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu		
35	200	205	210
	Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr		
	215	220	225
	Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp		
40	230	235	240
	Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro		
	245	250	255
45	Pro		
	256		

(2) INFORMATION FOR SEQ ID NO:71:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 452 amino acids
 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

	Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly		
	1	5	10
60	Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Ser Phe Ser		
	20	25	30

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	Ser	His	Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
					35					40						45
5	Glu	Trp	Val	Gly	Tyr	Ile	Asp	Pro	Ser	Asn	Gly	Glu	Thr	Thr	Tyr	
					50					55						60
	Asn	Gln	Lys	Phe	Lys	Gly	Arg	Phe	Thr	Leu	Ser	Arg	Asp	Asn	Ser	
					65					70						75
10	Lys	Asn	Thr	Ala	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	
					80					85						90
	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Gly	Asp	Tyr	Arg	Tyr	Asn	Gly	
15					95					100						105
	Asp	Trp	Phe	Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	
					110					115						120
20	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	
					125					130						135
	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	
					140					145						150
25	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	
					155					160						165
	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	
30					170					175						180
	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	
					185					190						195
35	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	
					200					205						210
	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	
					215					220						225
40	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	
					230					235						240
	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	
45					245					250						255
	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	
					260					265						270
50	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	
					275					280						285
	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	
					290					295						300
55	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	
					305					310						315
	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	
60					320					325						330
	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	
					335					340						345

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 350 355 360
 5 Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys
 365 370 375
 Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 380 385 390
 10 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
 395 400 405
 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
 15 410 415 420
 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu
 425 430 435
 20 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 440 445 450

Gly Lys
 452

25

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 219 amino acids
 30 (B) TYPE: Amino Acid
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

35 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
 1 5 10 15
 Gly Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Leu Val
 20 25 30
 40 His Gly Ile Gly Ala Thr Tyr Leu His Trp Tyr Gln Gln Lys Pro
 35 40 45
 Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe
 45 50 55 60
 Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 65 70 75
 50 Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
 80 85 90
 Tyr Tyr Cys Ser Gln Ser Thr His Val Pro Leu Thr Phe Gly Gln
 95 100 105
 55 Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val
 110 115 120
 Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala
 60 125 130 135
 Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys

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				140					145					150	
	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln
				155						160					165
5	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu
				170						175					180
	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys
10				185						190					195
	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val
				200						205					210
15	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys						
				215					219						